CLAIMS

We claim:

1. A method for determination of structure formation in nucleic acid targets, comprising the steps of:

a) providing:

i) a folded target having a deoxyribonucleic acid sequence comprising one or more double stranded regions, and one or more single stranded regions, and further comprising two or more non-contiguous portions, and one or more intervening regions; and

ii) one or more bridging oligonucleotide probes complementary to said two or more non-contiguous portions of said folded target; and

b) mixing said folded target and said one or more probes under conditions such that said probe hybridizes to said folded target to form a probe/folded target complex.

2. The folded target of Claim 1, wherein said one or more intervening regions comprises at least five nucleotides.

3. The method of Claim 1, further comprising detecting the presence of said probe/folded target complex.

4. The method of Claim 1, further comprising quantitating the amount of probe/folded target complex formed.

5. The method of Claim 1, wherein said probe in said probe/folded target complex is hybridized to at least one single stranded region of said folded target.

6. The method of Claim 3, wherein said bridging oligonucleotide probe further comprises a moiety that permits the capture of said bridging oligonucleotide probe by a solid support.

7. The method of Claim 6, wherein said detecting the presence of said probe/folded target complex comprises exposing said probe/folded target complex to a solid support under conditions such that said bridging oligonucleotide is captured by said solid support.

8. The method of Claim 7, wherein said moiety comprises a biotin moiety and said solid support comprises a surface having a compound capable of binding to said biotin moiety, said compound selected from the group consisting of avidin and streptavidin.

9. The method of Claim 1, wherein said folded target is labelled.

10. The method of Claim 3, wherein said folded target comprises a deoxyribonucleic acid sequence having a moiety that permits its capture by a solid support.

11. The method of Claim 10, wherein said detecting the presence of said probe/folded target complex comprises exposing said probe/folded target complex to a solid support under conditions such that said folded target is captured by said solid support.

12. The method of Claim 11, wherein said moiety comprises a biotin moiety and said solid support comprises a surface having a compound capable of binding to said biotin moiety, said compound selected from the group consisting of avidin and streptavidin.

13. The method of Claim 1, wherein said bridging oligonucleotide probe is labelled.

14. The method of Claim 1, wherein said bridging oligonucleotide probe is attached to a solid support.

15. The method of Claim 1, wherein said folded target nucleic acid is attached to a solid support.

16. A method for analyzing the structure of nucleic acid targets, comprising:

a) providing:

i) a first folded target having a nucleic acid sequence comprising first and second portions, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

iii) first and second bridging oligonucleotides said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and said second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and

iv) a solid support comprising first, second, third and fourth testing zones, each zone capable of capturing and immobilizing

said first and second bridging oligonucleotides;

b) contacting said first folded target with said first bridging oligonucleotide under conditions such that said first bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a first mixture;

c) contacting said first folded target with said second bridging oligonucleotide under conditions such that said second bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a second mixture;

d) contacting said second folded target with said first bridging oligonucleotide to form a third mixture;

e) contacting said second folded target with said second bridging oligonucleotide to form fourth mixture; and

f) adding said first, second, third and fourth mixtures to said first, second, third and fourth testing zones of said solid support, respectively, under conditions such that said first and second bridging oligonucleotides are captured and immobilized.

17. The method of Claim 16, wherein said first bridging oligonucleotide in step d) does not substantially hybridize to said second folded target.

18. The method of Claim 16, wherein the hybridization of said first bridging oligonucleotide in step d) to said second folded target is reduced relative to the hybridization of said first bridging oligonucleotide in step c) to said first folded target.

19. The method of Claim 16, wherein said first and second targets comprise DNA.

20. The method of Claim 16, wherein said first and second bridging oligonucleotides comprise DNA.

21. A method for analyzing folded nucleic acid targets, comprising:

a) providing:

i) a first folded target having a nucleic acid sequence comprising first and second portions, wherein said first and second portions each comprise one or more double stranded regions and one or more single stranded regions;

ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target, and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

iii) a solid support comprising first and second testing zones, each of said zones comprising immobilized first and second bridging oligonucleotides, said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and

b) contacting said first and second folded targets with said solid support under conditions such that said first and second bridging oligonucleotides hybridize to said first folded target to form a probe/folded target complex.

22. The method of Claim 21, wherein said contacting of step b) comprises adding said first folded target to said first testing zone and adding said second folded target to said second testing zone.

23. The method of Claim 21, wherein said first and second bridging oligonucleotides are immobilized in separate portions of said testing zones.

24. The method of Claim 23, wherein said first bridging oligonucleotide in said second testing zone does not substantially hybridize to said second folded target.

25. The method of Claim 23, wherein said first bridging oligonucleotide in said second testing zone hybridizes to said second folded target with a reduced efficiency compared to the hybridization of said first bridging oligonucleotide in first testing zone to said first folded target.

26. The method of Claim 21, wherein said first and second folded targets comprise DNA.

27. The method of Claim 21, wherein said first and second folded targets comprise RNA.

28. The method of Claim 21, wherein said first and second bridging oligonucleotides comprise DNA.